

Figure 1 Plasmid pCMV.Bx08.gp160

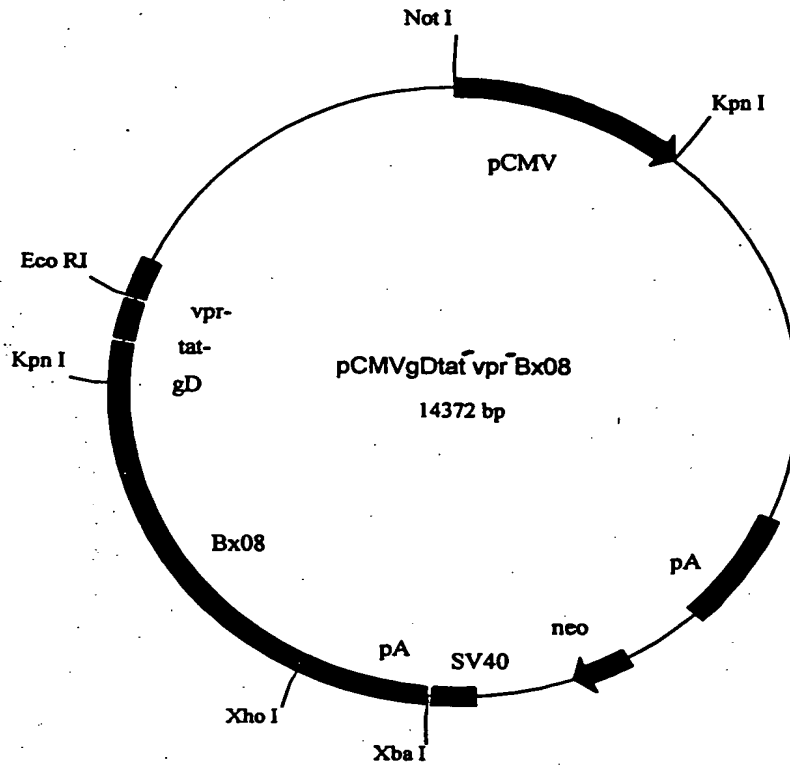


Figure 2 DNA immunization plasmid pCMV3Bx08.

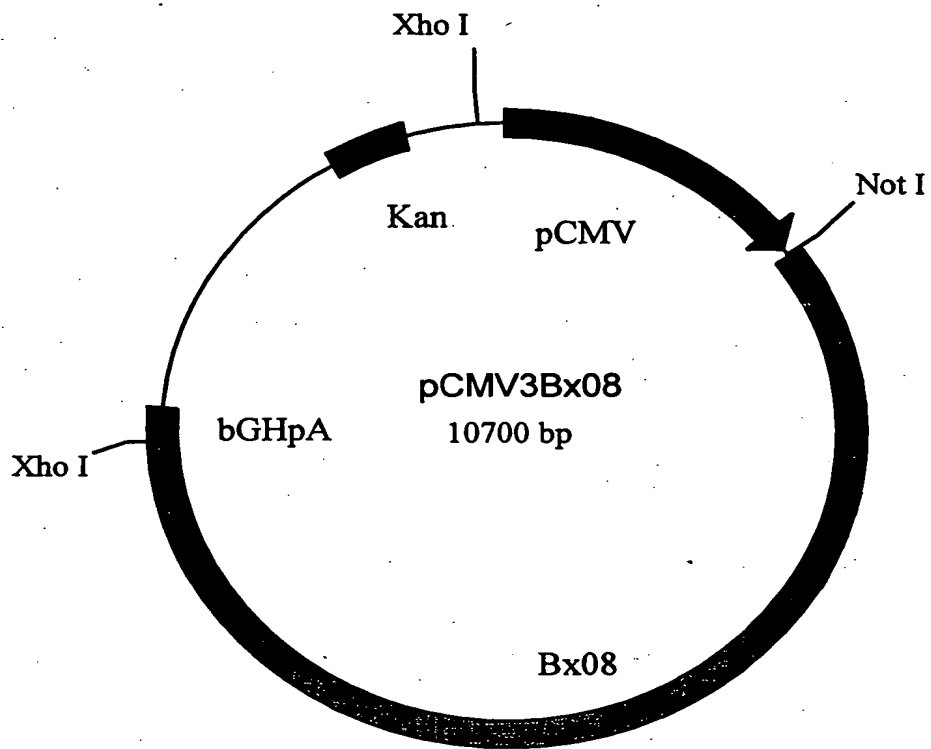


Figure 3. Pseudovirion Expression Plasmid p133B1 HIV-1 Bx08

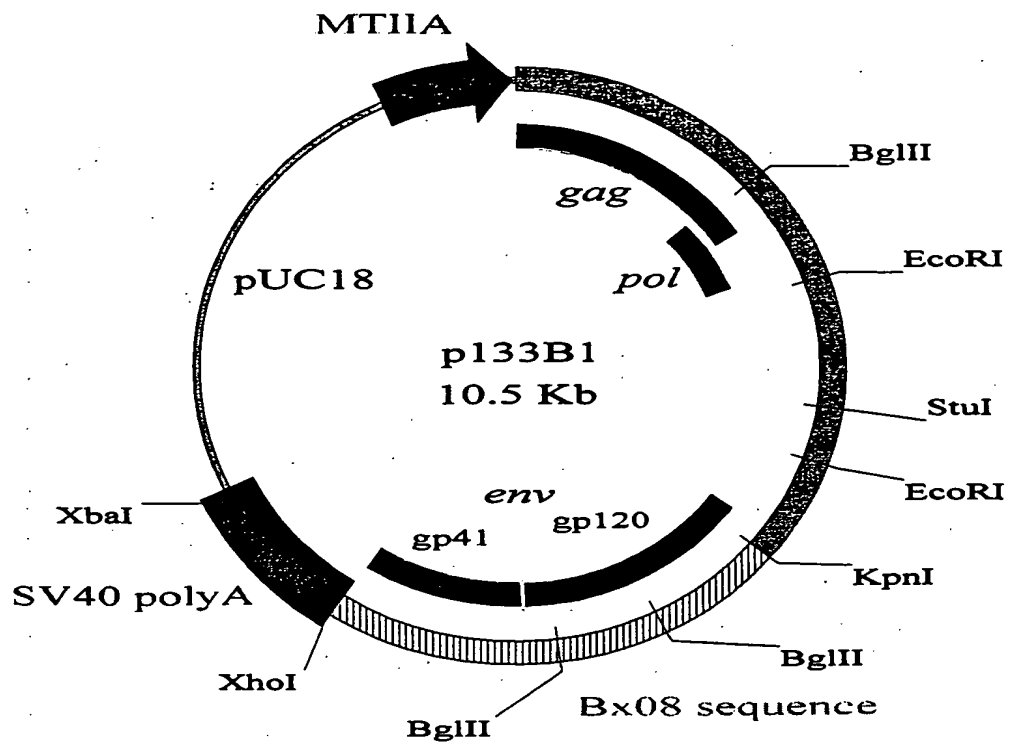


FIGURE 4

ALVAC(2)120(BX08)GNP

(vCP1579)

(ALVAC XhoI Restriction Map)

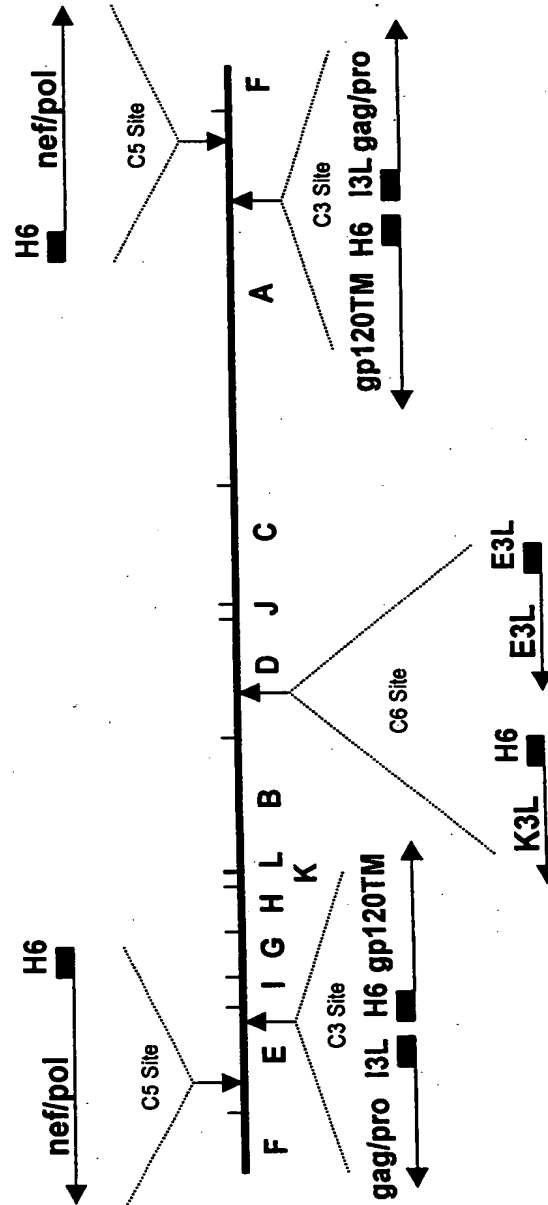


Figure 1: Time line of PMe-vaccine 1

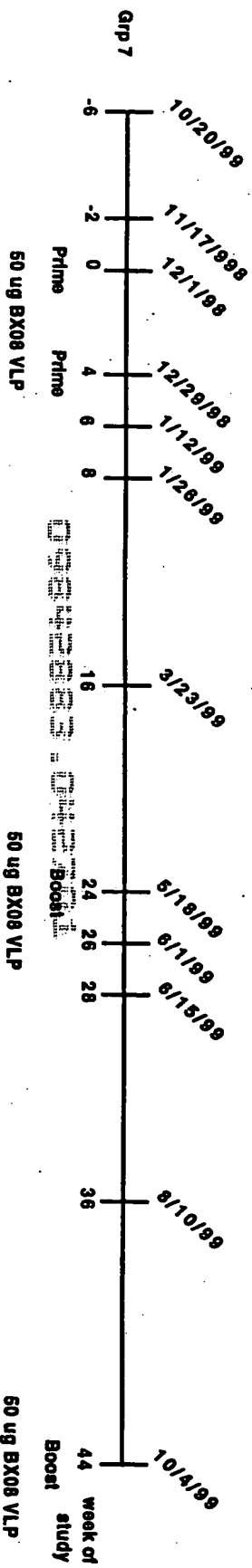
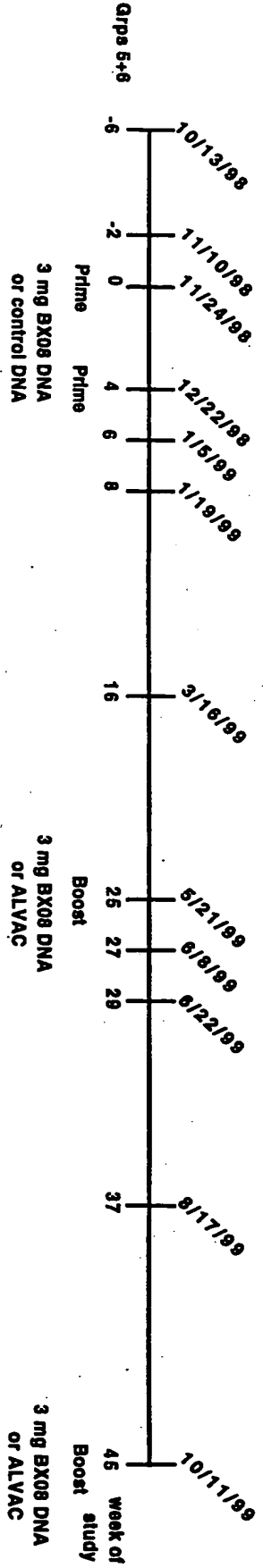
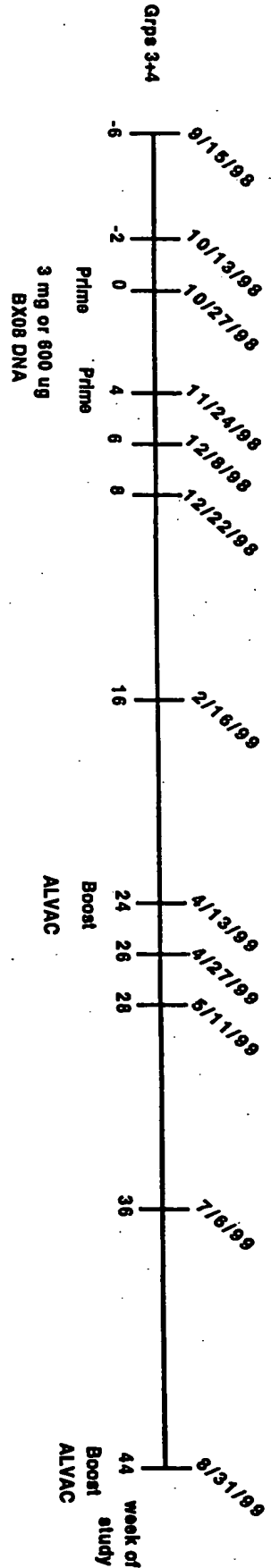
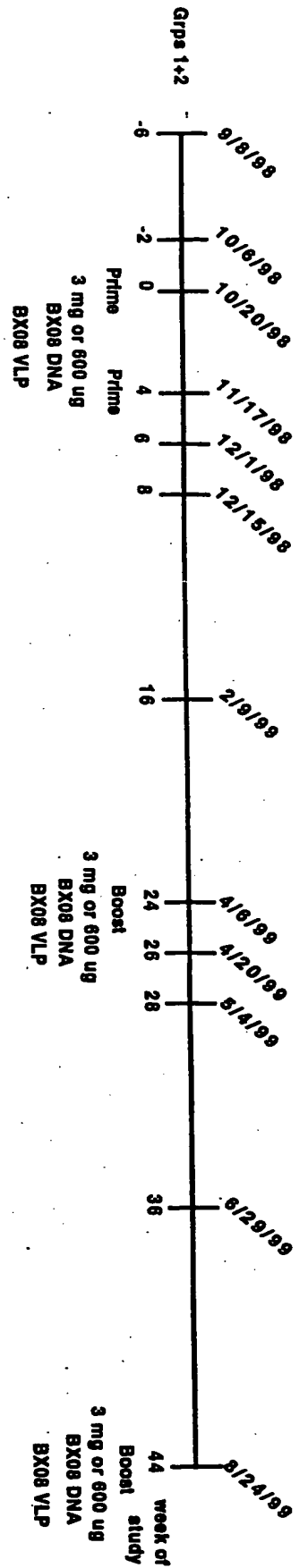
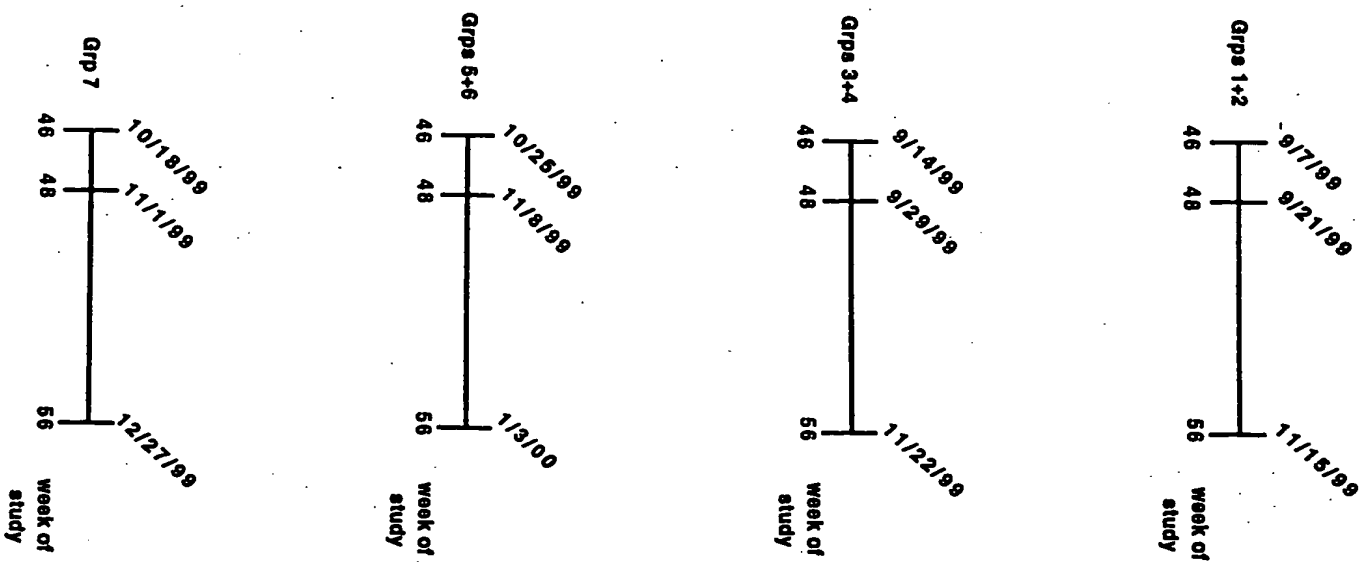
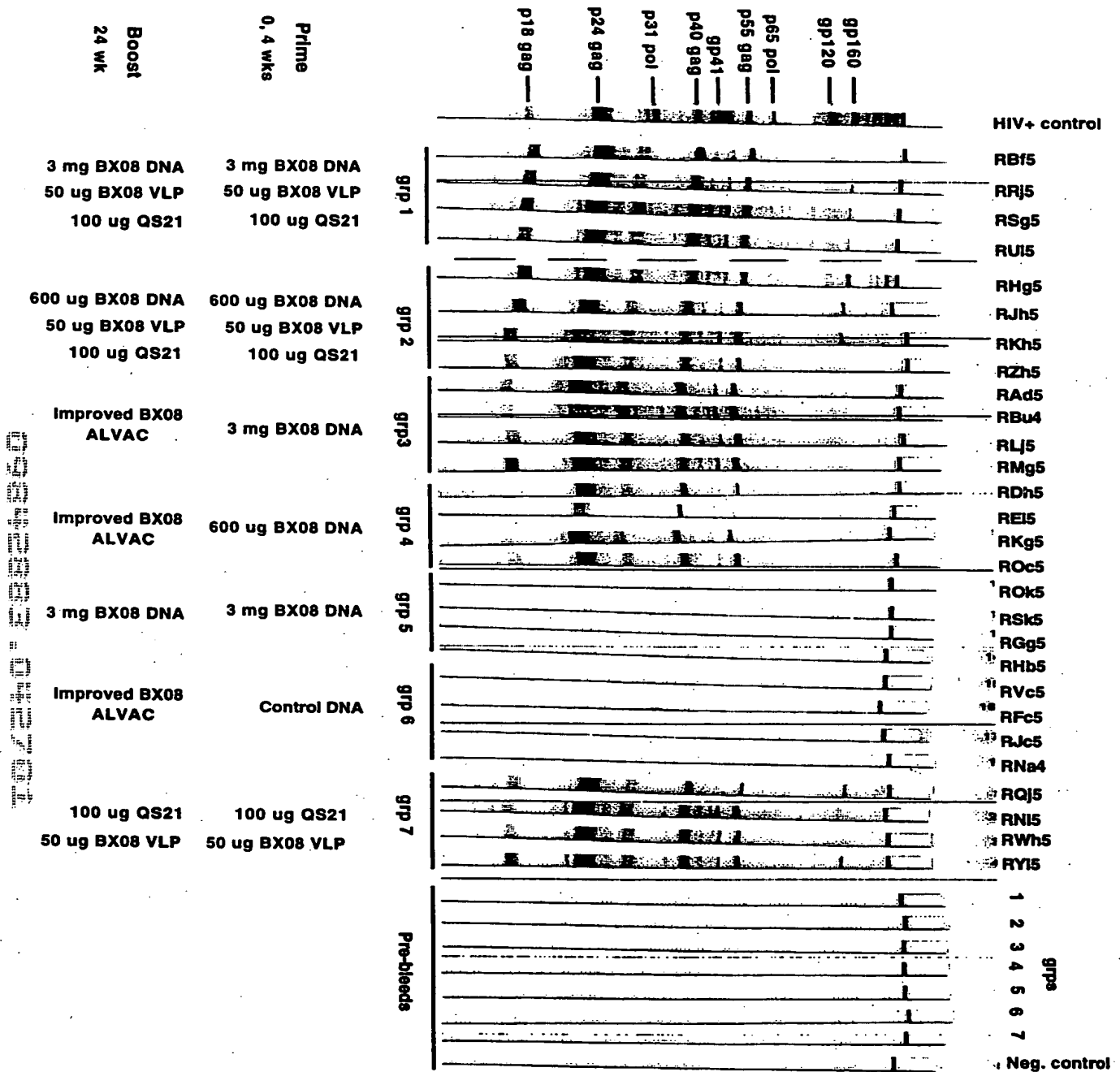


Figure 5 continued



week of
study

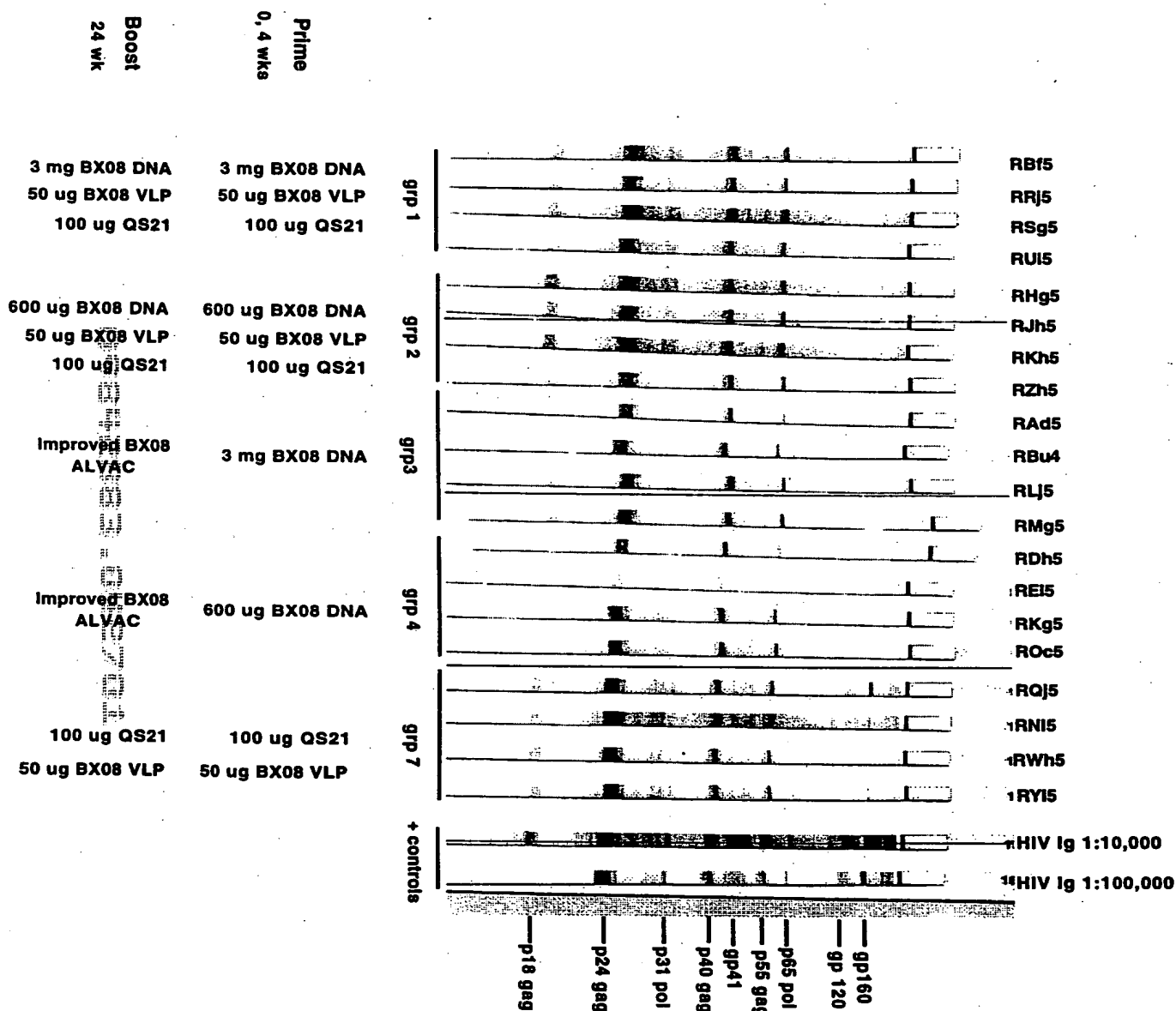
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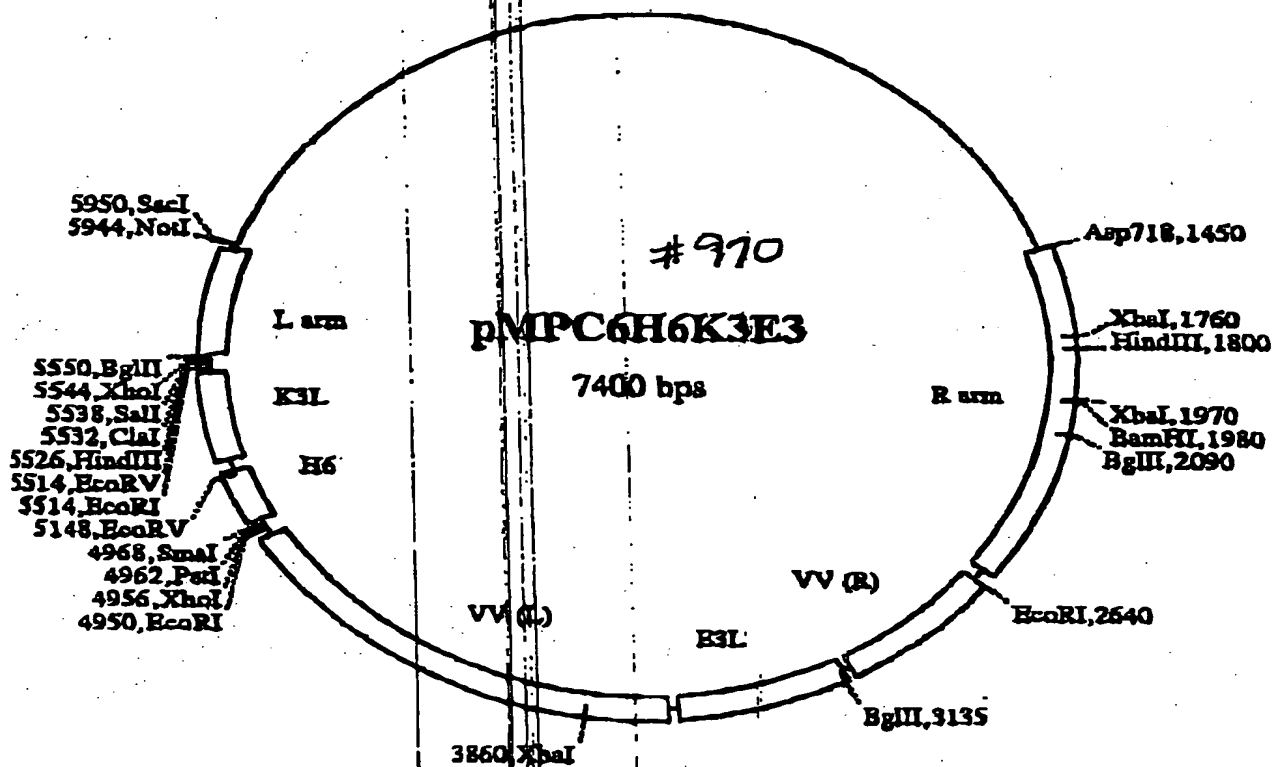
Figure 3: 26 wk macaque serum immunoreactivity to HIV antigens (1:1000 diln)



9/15

2-14-Pox R

Fig 8



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2-110-HIV

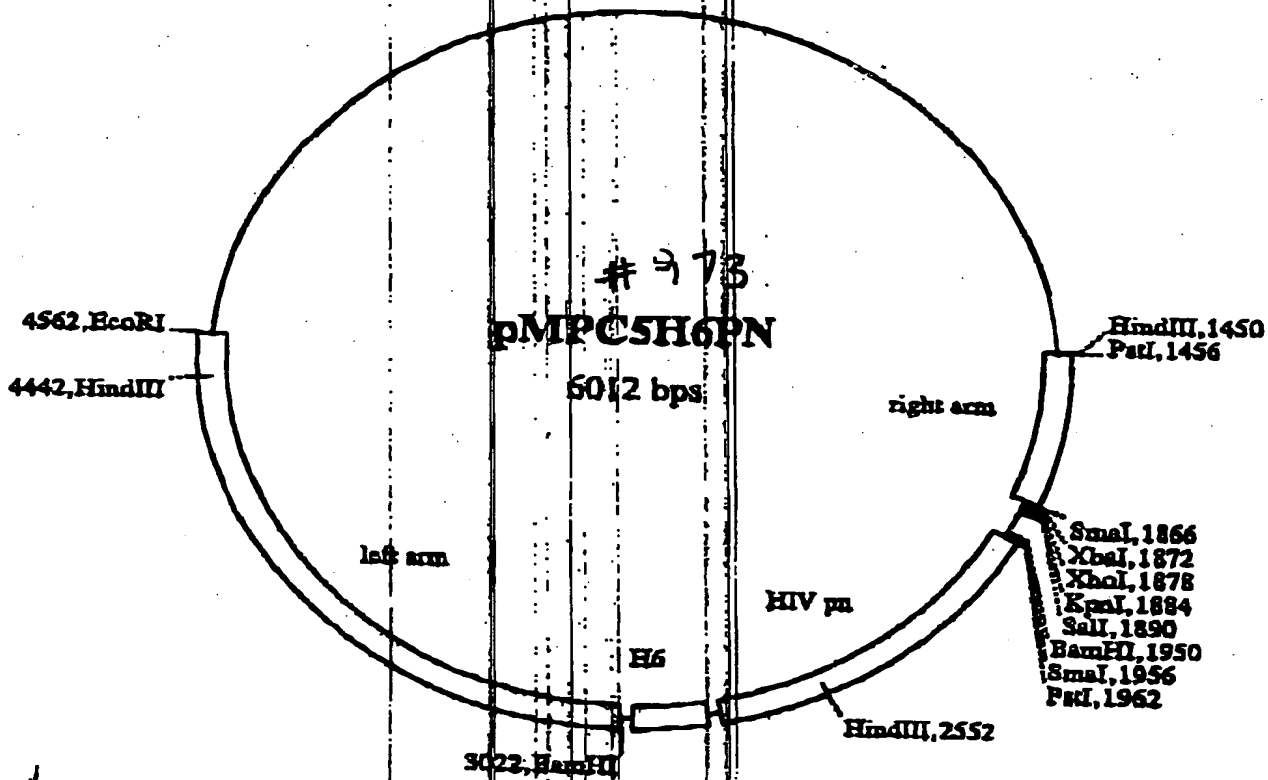


Figure 10 Plasmid pHIV76

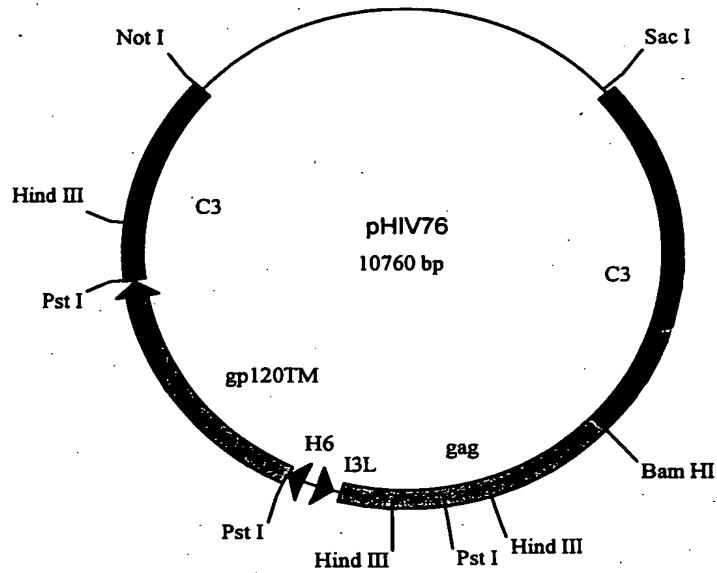


Figure 11

vCP1579: H6/HIV Pol/Nef epitope cassette in ALVAC C5 site

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61 GTCATAAAAA CCCGGGATCG ATTCTAGACT CGAGGGTACC GGATCTTAAT TAATTAGTCA
121 TCAGGCAGGG CGAGAACGAG ACTATCTGCT CGTTAATTAA TTAGGTCGAC GGATCCCCCA
181 ACAAAAACTA ATCAGCTATC GGGGTTAATT AATTAGTTAT TAGACAAGGT GAAAACGAAA
241 CTATTTGTAG CTTAATTAAT TAGAGCTTCT TTATTCTATA CTTAAAAAGT GAAAATAAAT
301 ACAAAGGTTT TTAGGGTTG TGTAAATTG AAAGCGAGAA ATAATCATAA ATTATTTTCAT
361 TATCGCGATA TCCGTTAAGT TTGTATCGTA ATGCCACTAA CAGAAGAAGC AGAGCTAGAA
421 CTGGCAGAAA ACAGAGAGAT TCTAAAAGAA CCAGTACATG GAGTGTATTA TGACCCATCA
481 AAAGACTTAA TAGCAGAAAT ACAGAAGCAG GGGCAAGGCC AATGGACATA TCAAATTTAT
541 CAAGAGCCAT TTAAAAATCT GAAAACAGGA ATGGAGTGGA GATTTGATTC TAGATTAGCA
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661 CAAAGTAGCA TGACAAAAAT CTTAGAGCCT TTTAGAAAAC AAAATCCAGA CATAGTTATC
721 TATCAATACA TGGATGATTT GTATGTAGGA TCTGACTTAG AAATAGGGCA GCATAGAACA
781 AAAATAGAGG AGCTGAGACA ACATCTGTTG AGGTGGGGAC TTACAACCAT GGTAGGTTTT
841 CCAGTAACAC CTCAAGTACC TTTAAGACCA ATGACTTACA AAGCAGCTGT AGATCTTTCT
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1261 TAATTAGTCA CGTACCTTTG AGAGTACCAC TTCAGCTACC TCTTTTGTGT CTCAGAGTAA
1321 CTTTCTTTAA TCAATTCCAA AACAG

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Upstream (right) flanking sequence: 1-266

VV H6 promoter: 267-390

HIV pol/nef/pol/nef/pol cassette: 391-1227

Downstream (left) flanking sequence: 1227-1345

Figure 12

E3L and K3L genes in C6

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      10      20      30      40      50      60      70      80      90      100     110
GAGCTCGCGG CCGCCTATCA AAAGTCTTAA TGAGTTAGGT GTAGATAGTA TAGATATTAC TACAAGGTA TTCATATTTC CTATCAATTC TAAAGTAGAT GATATTAATA
CTCGAGCGCC GCGCGATAGT TTTCAGAATT ACTCAATCCA CATCTATCAT ATCTATAATG ATGTTTCCAT AAGTATAAAG GATAGTTAAG ATTTTCATCTA CTATAATTAT

      120     130     140     150     160     170     180     190     200     210     220
ACTCAAAGAT GATGATAGTA GATAATAGAT ACGCTCATAT AATGACTGCA AATTGGGACG GTTCACATTT TAATCATCAC GCGTTCATAA GTTTCACCTG CATAGATCAA
TGAGTTTCTA CTACTATCAT CTATTATCTA TCGAGATATA TTAGTGACGT TTAACCTGCG CAAGGTGAAA ATTAGTAGTG CGCAAGTATT CAAAGTTGAC GTATCTAGTT

      230     240     250     260     270     280     290     300     310     320     330
AATCTCACTA AAAAGATAGC CGATGTATTT GAGAGAGATT GGACATCTAA CTACGCTAAA GAAATTACAG TTATAAATAA TACATAATGG ATTTTGTATT CATCAGTTAT
TTAGAGTGAT TTTTCTATCG GCTACATAAA CTCTCTCTAA CCTGTAGATT GATGCGATTT CTTTAATGTC AATATTTATT ATGTATTACC TAAAACAATA GTAGTCAATA

      340     350     360     370     380     390     400     410     420     430     440
ATTAAACATA AGTACAATAA AAAGTATTAA ATAAAAATAC TTACTTACGA AAAAATGACT AATTAGCTAT AAAAAACCAG ATCTCTCGAG GTCGACGGTA TOGATAAGCT
TAAATGTAT TCATGTTATT TTTCATAATT TATTTTATG AATGAATGCT TTTTACTGTA TTAATGATA TTTTGGGTC TAGAGAGCTC CAGCTGCCAT AGCTATTGCA

      450     460     470     480     490     500     510     520     530
TGATATCGAA TTCATAAAAA TT A TTG ATG TCT ACA CAT CCT TTT GTA ATT GAC ATC ATA TCC TTT TGT ATA ATC AAC TCT AAT CAC TTT
ACTATAGCTT AAGTATTTTT AA T AAC TAC AGA TGT GTA GGA AAA CAT TAA CTG TAG ATA TAT AGG AAA ACA TAT TAG TTG AGA TTA GTG AAA
<Q H R C M R K Y N V D I Y G K T Y D V R I V K
-----K3L-----

      540     550     560     570     580     590     600     610     620
AAC TTT TAC AGT TTT CCC TAC CAG TTT ATC CCT ATA TTC AAC ATA TCT ATC CAT ATG CAT CTT AAC ACT CTC TGC CAA GAT AGC TTC AGA
TTG AAA ATG TCA AAA GGG ATG GTC AAA TAG GGA TAT AAG TTG TAT AGA TAG GTA TAC GTA GAA TTG TGA GAG ACG GTT CTA TCG AAG TCT
<V K V T K G V L K D R Y E V Y R D M H M K V S E A L I A E S
-----K3L-----

      630     640     650     660     670     680     690     700     710
GTG AGG ATA GTC AAA AAG ATA AAT GTA TAG AGC ATA ATC CTT CTC GTA TAC TCT GCC CTT TAT TAC ATC GCC CGC ATT GGG CAA CGA ATA
CAC TCC TAT CAG TTT TTC TAT TTA CAT ATC TCG TAT TAG GAA GAG CAT ATG AGA CGG GAA ATA ATG TAG CGG GCG TAA CCC GTT GCT TAT
<H P Y D F L Y I Y L A Y D K E Y V R G K I V D G A N P L S Y
-----K3L-----

      720     730     740     750     760     770     780     790     800     810
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TGT TTT ACG TTC GTA TGC TATGTTGAA TTGCGTATAG CGCTATTACT TTATTAATAA CTAATAAAGA GCGAAAGTTA AATTGTGTTG GGAGTTCTTG
<C F A L M
-----K3L-----

      820     830     840     850     860     870     880     890     900     910     920
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GAAACATAAA TAAAAGTGAA AAATTCATAT CTTATTCTCT TCGAGATTAA TTAATTACTT GTCTAACAAA GCAAAAGGGG AACCGCATAG TGATTAATTA ATTGGGCCCG

      930     940     950     960     970     980     990     1000    1010    1020    1030
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      1150    1160    1170    1180    1190    1200    1210    1220    1230    1240    1250
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      1260    1270    1280    1290    1300    1310    1320    1330    1340    1350    1360
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TAAGGGTTCA GAAGTCAAGA TAGAAGATT TTTAGAAGTT GCATACCTTA TATTATTAGA TAAATGGAG AAGACTATAG TAATTACTAT ATCAAAAACCT GTGATAGAAG

      1370    1380    1390    1400    1410    1420    1430    1440    1450    1460    1470
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      1480    1490    1500    1510    1520    1530    1540    1550    1560    1570    1580
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-----E3L-----

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-----E3L-----

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<D I I V D A M A D A D P K D A E T T M F W R P P I D D S S Y
-----E3L-----

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-----E3L-----

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3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980
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GACTTTGCTA GATGTCTGAG TTGATACGTT CCTTATTGCT TATACGGTTA ATACAGATTA TAAAATTGAA ATCTTGATTT TGCAAGATGG TTATGATTTT TATCCTATGC

4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420
TGATAGGCTG TTAAAGCTG CAATAAATAG TAAGGATGTA GAAGAAATAC TTTGTTCTAT ACCTTCCGAG GAAAGAACTT TAGAACAACT TAAGTTTAAAT CAAACTTGTA
ACTATCCGAC AATTTTCGAC GTTATTATC ATTCCTACAT CTCTTTTATG AAACAAGATA TGGAAAGCTC CTTTCTTGAA ATCTTGTTGA ATTCAAATTA GTTTGAACAT

4430
TTTATGAAGG TACC
AAATACCTCC ATGG